

*Amendments to the Specification*

Please replace paragraph [0070] with the following new paragraph:

[0070] In another method, the actual frequencies of the codons are distributed randomly throughout the coding sequence. Thus using this method for optimization, if a hypothetical polypeptide sequence had 100 leucine residues, referring to Table 2 for frequency of usage in the humans, about 7, or 7% of the leucine codons would be UUA, about 13, or 13% of the leucine codons would be UUG, about 13, or 13% of the leucine codons would be CUU, about 20, or 20% of the leucine codons would be CUC, about 7, or 7% of the leucine codons would be CUA, and about 41, or 41% of the leucine codons would be CUG. These frequencies would be distributed randomly throughout the leucine codons in the coding region encoding the hypothetical polypeptide. As will be understood by those of ordinary skill in the art, the distribution of codons in the sequence will can vary significantly using this method, however, the sequence always encodes the same polypeptide. Three different human codon-optimized nucleotide sequences encoding native PA (GenBank Accession Number AAA2263 (SEQ ID NO:4)) which have been optimized using this method are presented herein as SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:25. Three different human codon-optimized sequences encoding native LF (GenBank Accession Number AAA22569 (SEQ ID NO:12)) which have been optimized using this method are presented herein as SEQ ID NO: 26, SEQ ID NO: 27 and SEQ ID NO: 28 ~~SEQ ID NO:21 and SEQ ID NO:22~~, respectively.